

P 5 10:01:16 2002

us-09-052-089a-5.rsp

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: September 4, 2002, 16:16:07 ; Search time 172.18 seconds
(without alignments)
51.241 Million cell updates/sec

Title: US-09-052-089a-5
Perfect score: 286
Sequence: 1 RALCTCSDPFDHSDVAAM.....IOSFETAPSRTPCPCRIQVG 51

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriaph:*
17: SP-archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	275	96.2	469	4 O00467	O00467 homo sapien
2	268	93.7	223	11 Q922M8	Q922M8 mus musculu
3	268	93.7	469	4 Q9BWF2	Q9BWF2 homo sapien
4	268	93.7	470	11 Q9CPD4	Q9CPD4 mus musculu
5	260	90.9	433	13 Q08854	Q08854 mus musculu
6	225	78.7	433	13 Q9YGN2	Q9YGN2 fugu rubrip
7	114	39.9	310	10 Q82372	Q82372 arabidopsis
8	114	39.9	420	4 Q75866	Q75866 homo sapien
9	114	39.9	420	4 Q95885	Q95885 drosophila
10	114	39.9	435	5 Q9Y8D7	Q9Y8D7 drosophila
11	113	39.5	158	5 Q9X2S4	Q9X2S4 drosophila
12	112	39.2	325	10 Q9M908	Q9M908 arabidopsis
13	109.5	38.3	263	5 Q95R85	Q95R85 drosophila
14	107	37.4	349	10 Q9N3D1	Q9N3D1 caenorhabdi
15	106	37.1	344	10 Q947X9	Q947X9 oryza sativ
16	103	36.0	344	10 Q65594	Q65594 arabidopsis

17	103	36.0	386	10 Q9L714	Q9L714 arabidopsis
18	102	35.7	324	10 Q82239	Q82239 arabidopsis
19	102	35.7	327	11 Q9DAH2	Q9DAH2 mus musculu
20	101	35.3	274	10 Q9L210	Q9L210 arabidopsis
21	100	35.0	224	10 Q9K907	Q9K907 arabidopsis
22	100	35.0	285	10 Q9ZTM6	Q9ZTM6 petunia hyb
23	99	34.6	524	10 Q9KAT1	Q9KAT1 arabidopsis
24	98	34.6	1181	5 Q97260	Q97260 plasmodium
25	98	34.3	325	10 Q9L708	Q9L708 arabidopsis
26	98	34.3	368	10 Q944L9	Q944L9 arabidopsis
27	98	34.3	383	10 Q9LMT3	Q9LMT3 arabidopsis
28	98	34.3	396	10 Q9FM98	Q9FM98 drosophila
29	98	34.3	621	5 Q9V9T8	Q9V9T8 drosophila
30	98	34.3	626	5 Q95SP2	Q95SP2 arabidopsis
31	97	33.9	291	10 Q9FEP6	Q9FEP6 mus musculu
32	96.5	33.7	243	11 Q99P05	Q99P05 oryza sativ
33	96.5	33.7	439	10 Q94GM2	Q94GM2 avyena fatua
34	95.5	33.6	442	10 Q9MAC5	Q9MAC5 homo sapien
35	95.5	33.4	504	4 Q9P004	Q9P004 homo sapien
36	95.5	33.4	506	10 Q9M143	Q9M143 arabidopsis
37	95	33.2	351	10 Q9ZV08	Q9ZV08 homo sapien
38	94	32.9	137	4 Q9NSR1	Q9NSR1 homo sapien
39	94	32.9	299	10 Q942E6	Q942E6 oryza sativ
40	94	32.9	879	13 Q90ZT8	Q90ZT8 gallus gall
41	94	32.9	923	13 Q90ZT7	Q90ZT7 xenopus lae
42	93	32.5	989	11 Q99ML9	Q99ML9 mus musculu
43	93	32.5	230	10 Q9FN35	Q9FN35 mus musculu
44	93	32.5	551	3 Q98109	Q98109 saccharomyc
45	92.5	32.3	408	5 Q01482	Q01482 caenorhabdi

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	469 AA.
000467			
ID	O00467		
AC	O00467		
DT	01-JUL-1997 (TREMBLrel. 04, Created)		
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	HTIRIP.		
GN	Homo sapiens (Human).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97258620; PubMed=9104814;		
RT	Lee S.Y., Lee S.Y., Choi Y.,		
RT	"TRAF-Interacting protein (TRIP): a novel component of the tumor		
RT	necrosis factor receptor (TNFR) - and CD30-TRAF signaling complexes		
RT	that inhibits TNFR2-mediated NF-kappaB activation."		
RT	J. Exp. Med. 185:1275-1285(1997).		
CL	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
CC	EMBL: U77845; AAB22933.1; -		
DR	InterPro: IPR001841; Znf_Fing.		
DR	InterPro: IPR001841; Znf_Fing.		
DR	SMART: SM00184; RING; 1.		
DR	SMART: SM00184; RING; 1.		
KW	ZINC-finger.		
SO	SEQUENCE		
Query Match	96.2%; Score 275; DB 4; Length 469;		
Best local similarity	96.1%; Pred. No. 1.2e-29;		
Matches	49; Conservative		
QY	1 RALCTCSDPFDHSDVAAMCGHTFHLCILIOSFETAPSRTPCPCRIQVG 51		
DB	4 RALCTCSDPFDHSDVAAMHGGHTFHLCILIOSFETAPSRTPCPCRIQVG 54		
	Matches 49; Mismatches 1; Indels 0; Gaps 0;		

KA Lee S.H., Lee S.H.: "TRAF-interacting protein (TRIP): a novel component of the tumor
RT "TRAF-interacting protein (TRIP): a novel component of the tumor
RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
RT that inhibits TRAF2-mediated NF-kappaB activation.";
RL J. Exp. Med. 185:1275-1285(1997).
CC I. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: U77844; AAB5294.1; -.
DR MGD: MGI:1096377; Tralp.
DR InterPro: IPR001841; Znf_rtnlg

DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SO SEQUENCE 470 AA; 53191 MW; 00FD705B52645133 CRC64;

Query Match
Best Local Similarity 90.9%; Score 260; DB 11; Length 470;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALCTICSDPFDRHSDVAAMDCGTHFLQCLIOSFEFTAPSRCTCQCRIOV 51
Db 5 SLCTICSDPFDRHSDVAAMDCGTHFLQCLIOSFEFTAPSRCTCQCRIOV 54

RESULT 6
QY9GN2 PRELIMINARY; PRT; 433 AA.
AC QY9GN2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN TRAF INTERACTING PROTEIN.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99148833; PubMed-10025966;
RA Cottage A.J., Clark M., Hawker K., Umrana Y., Wheller D., Bishop M.,
RA Elger G.;
RT "Three receptor genes for plasmalogen related growth factors in the
RT genome of the puffer fish Fugu rubripes.";
RL FEBS Lett. 443:370-374(1999).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AJ010317; CA09084.1;
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SO SEQUENCE 433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;

Query Match
Best Local Similarity 78.7%; Score 225; DB 13; Length 433;
Matches 38; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 RALCTICSDPFDRHSDVAAMDCGTHFLQCLIOSFEFTAPSRCTCQCRIOV 50
Db 4 RAQCTICSDPFDRHSDVAAMDCGTHFLQCLIOSFEFTAPSRCTCQCRIOV 53

RESULT 7
ID 082372 PRELIMINARY; PRT; 310 AA.
AC 082372;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN ATG29840. PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;

RX MEDLINE-20083487; PubMed-10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden B., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carreira A.J., Greasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC005496; AAC35217.1;
DR HSSP: P28990; 1CHC.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SO SEQUENCE 310 AA; 35390 MW; EEEC1401152F5E2C CRC64;

Query Match
Best Local Similarity 39.9%; Score 114; DB 10; Length 310;
Matches 19; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

QY 3 LCTICSDPFDRHSDVAAMDCGTHFLQCLIOSFEFTAPSRCTCQCRIOV 50
Db 260 MCSICLIEFDGSRVALPCGHEFDECAKWFET--NHDCPLCRFKL 305

RESULT 8
ID 075866 PRELIMINARY; PRT; 420 AA.
AC 075866;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE R31343.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garves J.,
RA Dangaran L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Atlix C., Andreise T., Trankheim M., Amico-Keller G., Coeffield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 2.5 Mb region in 19p13.3.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC005764; AAC62428.1;
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003137; PA.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF02225; PA; 1.
DR SMART: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS0186; EGF_2; UNKNOWN_1.
KW Zinc-finger.
SO SEQUENCE 420 AA; 45880 MW; 572731A8EA97FCE CRC64;

Query Match
Score 39.9%; Score 114; DB 4; Length 420;

Best Local Similarity 37.5%; Pred. No. 1,4e-07;
Matches 18; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

OY 3 CTTCSDFPHSRDYAMDCGHTFHLCLOLQSEPTAPSRPCPOCR 50
Db 299 LCAITCDEYBERGDKLTIPCSHTYHCKCIDPWEQOAPRRSCPCVKQSV 346

RESULT 9

O95SS5 PRELIMINARY; PRT; 435 AA.

AC O95SS5; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GH03577P.

GN CG5140.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RP SEQUENCE FROM N.A.

RC STRAIN=Y, CN BW SP;

RA Stappleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Chang M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacble J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,

RA Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.

RL EMBL: AY006010; AAL28158.1; -

DR SEQUENCE 435 AA; 48455 MW; 0BFF0AC81DD9416E CRC64;

Query Match 39.9%; Score 114; DB 5; Length 435;

Best Local Similarity 47.7%; Pred. No. 1.5e-07;

Matches 21; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

OY 4 CTTCSDFPHSRDYAMDCGHTFHLCLOLQSEPTAPSRPCPOCR 47

Db 6 CVICAEILFGQADEVFATVCGHMFHNCINQWLDR--SKTCPOCR 47

RESULT 10

O9V8D7 PRELIMINARY; PRT; 455 AA.

AC O9V8D7; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CG5140. PROTEIN.

GN CG5140.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA April J.F., Agbayani A., An H.-J., Andrews-Plannkoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Padlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jatalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacble J.M.,

RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reiner K., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spredling A.C., Stappleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wattarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage F., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL: AED03800; AAF57730.1; -

DR FLYbase: FBgn0034314; CG5140.

DR InterPro: IPR001841; Znf_ring.

DR Pfam: PF00097; zfc3HC4; 1.

DR SMART: SM00184; RING; 1.

KW Zinc-finger.

SO SEQUENCE 455 AA; 50726 MW; BEA74FACACE8FD5B CRC64;

Query Match 39.9%; Score 114; DB 5; Length 455;

Best Local Similarity 47.7%; Pred. No. 1.5e-07;

Matches 21; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

OY 4 CTTCSDFPHSRDYAMDCGHTFHLCLOLQSEPTAPSRPCPOCR 47

Db 6 CVICAEILFGQADEVFATVCGHMFHNCINQWLDR--SKTCPOCR 47

RESULT 11

O9XZS4 PRELIMINARY; PRT; 158 AA.

AC O9XZS4; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE EG:22E5.12 OR CG4325.

GN EG:22E5.12 OR CG4325.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA April J.F., Agbayani A., An H.-J., Andrews-Plannkoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Padlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Domes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslcr C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Kaipen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matell B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.Y., Mobarry C., Morris J., Moshireli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Put V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).

RP SEQUENCE FROM N.A.
RA Murphy L., Harris D., Barrell B.;
RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RA Benos P.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AE003422; AAF45708.1; -;
DR EMBL: AL031765; CAB41708.1; -;
DR FLYBase: FBgn0026878; EG:22E5.12.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; Zf-C3HC; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 158 AA; 17741 MW; 21C417B040642D73 CRC64;

Query Match 39.5%; Score 113; DB 5; Length 158;
Best Local Similarity 48.9%; Pred. No. 7.2e-08;
Matches 23; Conservative 4; Mismatches 18; Indels 2; Gaps 1;
OY 3 LCTICSDFFDHSRDV--AAMDGHTFHLOCLIOSEFETAPSTPCQCRIO 49
DB 7 ICTICSEFRITSDNIOAGSGHAFHEDCL--DHWKQSRTPCICHSQ 51

RESULT 12
O9M9U8 PRELIMINARY; PRT; 325 AA.
AC O9M9U8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE F6A14.12 (TREMblrel. 19, Last annotation update)
DE F6A14.12 PROTEIN.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

RP SEQUENCE FROM N.A.
RA Federpiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Kowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shin P., Toriumi M., Vystotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC011809; AAF27102.1; -;
DR InterPro: IPR001664; IF.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00226; IF; UNKNOWN_1.
KW Zinc-finger.
SQ SEQUENCE 325 AA; 36919 MW; 837FDB7F28F2B615 CRC64;

Query Match 39.2%; Score 112; DB 10; Length 325;
Best Local Similarity 37.5%; Pred. No. 2.1e-07;
Matches 18; Conservative 11; Mismatches 17; Indels 2; Gaps 1;
OY 3 LCTICSDFFDHSRDV--AAMDGHTFHLOCLIOSEFETAPSTPCQCRIO 50
DB 276 VCTICLEFDDGSRIVTLPCGHEFDECEVLEWF--VRSHVCPCLRUCL 321

RESULT 13
O95RB5 PRELIMINARY; PRT; 263 AA.
AC O95RB5;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ID46221P.
GN CG10916.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Y, CN BW SP;
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farlan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.R., Rubin G.M., Celinker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY061504; AAL29052.1; -;
SQ SEQUENCE 263 AA; 29515 MW; B98CECE994071BFF CRC64;

Query Match 38.3%; Score 109.5; DB 5; Length 263;
Best Local Similarity 46.8%; Pred. No. 3.7e-07;
Matches 22; Conservative 6; Mismatches 14; Indels 5; Gaps 3;
OY 3 LCTICSDFFDHSRDV--AAMDGHTFHLOCLIOSEFETAPSTPCQCR 47
DB 31 LCAICNEFF-RANDIFSTSRGSHVFKDCLTRMLNR--SRTCPQCR 74

RESULT 14
O9N3D1 PRELIMINARY; PRT; 304 AA.
AC O9N3D1;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE HYPOTHEICAL 33.4 KDA PROTEIN.
GN y54E10BR.3.
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode *C. elegans*: a platform for
investigating biology." The *C. elegans* Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Tln-Mollam A., Becker M., Graves T.;
RT "The sequence of *C. elegans* cosmid Y54E10B8.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AC024812; AAE9555.1; -;
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KW Hypothetical protein; Zinc-finger.
SQ SEQUENCE 304 AA; 33447 MW; 3E522361A5F54C44 CRC64;

Query Match 37.4%; Score 107; DB 5; Length 304;
Best Local Similarity 42.9%; Pred. No. 9.4e-07;
Matches 21; Conservative 5; Mismatches 21; Indels 2; Gaps 1;
OY 2 AICTCSDFDHSRDYAAADCCHTFLQCLIOSFETAPSRCPQCRIOV 50
DB 236 AACTCTCFDFKLEDEVDGALDCNHIFRPFCEPWLKT--KNSCPVCROKV 282
RESULT 15
OY 0947X9 PRELIMINARY; PRT; 349 AA.
ID 0947X9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHEICAL 39.6 KDA PROTEIN.
GN OSJNBA0067N01.18.
GN Oryza sativa (Rice).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIPPONBARE;
RA de la Bastide M., Spiegel L., Preston R., Kirchoff K., King L.,
RA Nascimeto L., Baker J., Vil M.D., Zulfavren T., Santos L., Miller B.,
RA Kuit K., Cunnius D.M., Rodriguez S., Ballja V., Shah R., Bahret A.,
RA Yang C., Bell M., Palmer L., O'Shaughnessy A., Dedha N.,
RA McCumle W.R.;
RT "Genomic Sequence for *Oryza sativa*, Nipponbare strain, clone
OSJNBA0067N01, from chromosome 3, complete sequence.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC090485; AAK98739.1; -;
KW Hypothetical protein.
SQ SEQUENCE 349 AA; 39557 MW; ECF2CDC80CCE2DE1 CRC64;

Query Match 37.1%; Score 106; DB 10; Length 349;
Best Local Similarity 38.6%; Pred. No. 1.5e-06;

Matches 17; Conservative 12; Mismatches 13; Indels 2; Gaps 2;
OY 4 CTICSDFFDHSRDYAAADCCHTFLQCLIOSFETAPSRTPQC 46
DB 212 CPVCEYELFDSTKDISALHCGHTHLECLYE--MRSHQOFCPCVC 254

RESULT 16
ID 065594 PRELIMINARY; PRT; 344 AA.
AC 065594;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHEICAL 38.7 KDA PROTEIN.
GN M3E9.170 OR AT4G26400.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Vandenberg M., Jallet C., Portetelle D., Hohnsels J.,
RA Mewes H.W., Mayer K., Schueller C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 65-344 FROM N.A.
RA rose M., Hempel S., Ertlan K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Vandenberg M., Jallet C., Portetelle D., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AL022223; CA18230.1; -;
DR EMBL; AL161565; CAB79495.1; -;
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KW Hypothetical protein; Zinc-finger.
SQ SEQUENCE 344 AA; 36720 MW; EB31D0BF5EDA700 CRC64;

Query Match 36.0%; Score 103; DB 10; Length 344;
Best Local Similarity 38.3%; Pred. No. 3.8e-06;
Matches 18; Conservative 8; Mismatches 19; Indels 2; Gaps 1;
OY 4 CTICSDFFDHSRDYAAADCCHTFLQCLIOSFETAPSRTPCPCRIQV 50
DB 229 CSTCLDDPDKGSEAKEMPCFKHFRICLVPELHSS--CPVCYVEL 273

RESULT 17
ID 09LT14 PRELIMINARY; PRT; 386 AA.
AC 09LT14;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 3, PL CLONE: MPV9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

	Query Match	35.7%	Score 102;	DB 10;	Length 324;
	Best Local Similarity	41.3%;	Pred. No. 4.9e-06;		
	Matches 19;	Conservative 6;	Mismatches 19;	Indels 2;	Gaps 1
Oy	4 CTIC--SDFFHDSRDVAAADCGHTTFLQCLIOSFETAPSRTPCPCR 47				
	: : : : : :				
Dd	38 CSTLESYLDDGTGRSKATKIOGCHPHLDCIGSAFMNKGAMGPCNR 83				
	: : : : : :				
	RESULT 19				
	O9DAH2	PRELIMINARY:	PRT:	327 AA.	
AC	O9DAH2:				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	SPPRMTID SPECIFIC RING ZINC FINGER 1.				
CS	SSRF1.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
NX	NCBI_TaxId=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=TESTIS;				
XC	MEDLINE=21085660; PubMed=1121785j;				
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,				
RA	Aikawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., Ring B., Kochwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,				
RA	Lions P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Konttski S.,				
RA	Hayashizaki Y.;				
RT	"Functional annotation of a full-length mouse cDNA collection";				
RL	Nature 409:685-690(2001).				
CC	-I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.				
DR	HSP: AK005843; BAB24269.1; -				
DR	HSP: P28990; ICHC.				
DR	MGD: MG134128; Ssrzfl.				
DR	InterPro: IPR000561; EGF-like.				
DR	InterPro: IPR001841; Zn_f_ring.				
DR	Pfam: PF00097; zf-C3HC4; 1.				
DR	SMART: SMO0184; RING: 1.				
DR	PROSITE: PS01186; EGF_2; UNKNOWN_1.				
DR	Zinc-finger.				
KQ	SEQUENCE 327 AA; 35627 MW; 5F8D34ABEE394193 CRC64;				
	Query Match	35.7%	Score 102;	DB 11;	Length 327;
	Best Local Similarity	33.3%;	Pred. No. 4.9e-06;		
	Matches 16;	Conservative 9;	Mismatches 23;	Indels 0;	Gaps 0;
OY	3 LCITCSDFDHSRDVAAADCGHTTFLQCLIOSFETAPSRTPCPCR 50				
	: : : : : :				
Dd	208 LCAITCIDDYEGGERLKTIPLCAHAHYHCRCDIPWFSAARSCSPLCKRSV 255				
	: : : : : :				
	RESULT 20				
ID	O9LZ10	PRELIMINARY:	PRT:	274 AA.	

DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE HYPOHECTICAL 31.1 KDA PROTEIN.
GN Pgcl4_60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eumariophyta: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RP Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Meyer K.F.X.;
RP Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AL162973; CAB86029.1; -
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1
DR Hypothetical protein; Zinc-finger.
SQ SEQUENCE 274 AA: 31102 MW: 9698B6C495A6F068 CRC64;

Query Match	35.3%;	Score 101;	DB 10;	Length 274;
Best Local Similarity	38.38%;	Pred. No. 5.6e-06;		
Matches 18; Conservative	6;	Mismatches 21;	Indels 2;	Gaps 1;

QY 4 CTICSDFFDHSRDVAAMDCGHTFHQLCLIQSFETAPSRTPQCRIQV 50
 | || : ||| | | | | | | | | | |
Db 205 CVICKKEEMSEGRDYCEMPCQHFTFWKCILPWL--SKNTCPFCRFL 24

RESULT	21	
09M9U7		
ID	09M9U7	PRELIMINARY;
		PRT; 224 AA

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DT      01-OCT--2000 (TREMBLrel. 15, Created)
DT      01-OCT--2000 (TREMBLrel. 15, last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE      F6A14.13 PROTEIN.
GN      F6A14.13.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC      Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Fiederspelt N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA      Alfatefi H., Araujo R., Hutzar D., Rowley D., Buehler E., Dunn P.,
RA      Gonzalez A., Kremenskaya I., Kim C., Lenz C., Li J., Liu S.,
RA      Lueros S., Schwartz J., Shim P., Toriumi M., Vysotskaya V.S.,
RA      Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL      Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC      EMBL: AC011809; AAF27103.1; -.
DR      HSSP; P28990; 1CHC.
DR      InterPro; IPRO03903; UIM.
DR      InterPro; IPRO01841; ZnF_r1ng.
DR      Pfam; PF00097; zf-C3HC4.1.
DR      SMART; SM00184; RING; 1.
DR      ZINC-finger.
SQ      SEQUENCE 224 AA: 26040 MW: 5639265745C61F8C CRC64:
KW

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Query Match	35.08;	Score 100;	DB 10;	Length 224;
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Best Local Similarity	38.3%;	Pred. No. 6.3e-06;
Matches	18;	Conservative 9;
		Mismatches 18;
		Indels 2;
		Gaps 1.

Oy 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSEETAPRTCPQCRIQV 50
||| : | : ||| : :: ||| : || || : :
Db 175 CTICLEEFNDGTAKVMPLPCGHFEDECEVLTFEET--NHDCPLCRFKL 219

RESULT 22

ID	Q92TM6	PRELIMINARY;	PRT;	285 AA
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01-MAY-1999 (TREMBLER, 10, Created)

DT	01-MAY-1999	(TREMBLER: 10, last sequence update)
ET	01-DEC-2001	(TREMBLER: 19, last annotation update)

DE PGPD14.

OS Petunia hybrida (Petunia)

Spermatophyta: Magnoliophyta

NCPT TAXID=A102.

RN [1]

RC TISSUE=GERMINATING PETUNIA POLLEN TREATED WITH KAEMPFEROL

BA GUYON V.N.; Astwood J.D.; Garner H

of flavonol-induced pollen germination in petunia."

Plant Physiol. 123:699-710(2000)

DR InterPro; IPR001841; Zn_f_ring.

SEQUENCE 285 AA; 32987 MM; B4D20BC86F1D3D86 CRC64;

Query Match	Score	ID	Length
33.08;	100,	22	100
35.48;	8e-06;		

Matches	16;	Conservative	12;	Mismatches	14;	Indels	2;	Gaps	2
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QY 4 CTTCDSF-FDHSRDVAMDCGHTFHLCCLIOSEFTAPSRPCPC 46
| : : : : | | | | : : : : | : : : : |
Db 162 CPVCFEYFEDTNTIVLPICGHTMHECVNQ-MEQHNDISCPVC 204

RESULT	23	
Q9MAIL		
ID	Q9MAIL	PRELIMINARY;
		PRT;
		524 AA

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE F12M16.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
ON NCBI_TaxID=3702;
RX [1]
RP SEQUENCE FROM N.A.
RA Kim C., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Shinn P.,
RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
RA Hultzer L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S.,
RA Rowley D., Schwartz J., Tortum M., Vysotskaia V., Yu G., Davis R.W.,
RA Federspiel N.A., Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F12M16 from chromosome
I.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL, ACC08007; AAP69531.1; -;
DR InterPro: IPR001841; Znf_r1ng.
DR Pfam: PF000597; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.

DR SMART; SM00184; RING; L.


```
KW zinc-finger.
SQ SEQUENCE 524 AA; 58471 MW; CFC6AB4E39BD6FF CRC64;

Query Match
Best Local Similarity 34.6%; Score 99; DB 10; Length 524;
Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

Qy 4 CTICSDFFDHSRDVAAADCCHTFLHLOCLIOSFETAPSRTPCQCR 47
Db 472 CTICSESKNEKATATDCCHEHYAECLERKL--IVANVCPICK 513

RESULT 24
ID 097260 PRELIMINARY; PRT; 1181 AA.
AC 097260;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE HYPOTHETICAL 135.6 KDA PROTEIN.
GN PRC0610C, MAL3p5.8
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_Taxid=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Felwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrett B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum."
RL Nature 400:532-538(1999).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AL034556; CAB8971.1; -.
DR HSSP: P28990; ICNC.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Hypothetical protein; zinc-finger.
SQ SEQUENCE 1181 AA; 135638 MW; 288C44EA4FB8C2D4 CRC64;

Query Match
Best Local Similarity 34.6%; Score 99; DB 5; Length 1181;
Matches 16; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

Qy 4 CTICSDFFDHSRDVAAADCCHTFLHLOCLIOSFETAPSRTPCQCR 50
Db 1131 CCLICENYOHNDVNIPLCTHNFHKCCLIKWI--SKNTTCLCKIDL 1175

RESULT 25
ID 09LT08 PRELIMINARY; PRT; 325 AA.
AC 09LT08;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GB|AA27103.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AB024034; BAB02789.1; -.
DR HSSP: P28990; ICNC.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW zinc-finger.
SQ SEQUENCE 325 AA; 36432 MW; 694044F361053DE4 CRC64;

Query Match
Best Local Similarity 34.3%; Score 98; DB 10; Length 325;
Matches 18; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

Qy 4 CTICSDFFDHSRDVAAADCCHTFLHLOCLIOSFETAPSRTPCQCR 50
Db 275 CTICLEFNFAGGILVALPCGHDFDECAVWFET--NHFCPLCYREL 319

RESULT 26
ID 0944L9 PRELIMINARY; PRT; 368 AA.
AC 0944L9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ATG1970/F2H15.16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carlincl P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kaniya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF428290; AL16122.1; -.
SQ SEQUENCE 368 AA; 41618 MW; 79AD48BD0790A08E CRC64;

Query Match
Best Local Similarity 34.3%; Score 98; DB 10; Length 368;
Matches 15; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

Qy 4 CTICSDFFDHSRDVAAADCCHTFLHLOCLIOSFETAPSRTPCQCR 47
Db 320 CSICDVEYREDEVELGNCGHSHFVHCVKWL--SRKNACPVCK 361

RESULT 27
ID 09LMT3 PRELIMINARY; PRT; 363 AA.
AC 09LMT3;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GB|AA27103.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
```

DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE F2H15.19 PROTEIN.
GN F2H15.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sakano H., Liu S.X., Ergu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
RA Alatali H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
RA Nguyen M., Palm C.J., Shim P., Southwick A., Davis R.W., Ecker J.R.,
RA Federspiel N.A., Theologis A.;
RT "The sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC034106; AAF97276.1; -;
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger
SQ SEQUENCE 363 AA; 43262 MW; EE8ADEBE91FE0B224 CRC64;

Query Match 34.3%; Score 98; DB 10; Length 383;
Best Local Similarity 34.1%; Pred. No. 2e-05;
Matches 15; Conservative 11; Mismatches 16; Indels 2; Gaps 1;
OY 4 CTICSDFFDHSRDVAMDCGHTFHLCQCLIOSFETAPSTPCQCR 47
Db 335 CSICDREYERDEYELGNCSHFVHCYKQWL--SRKNACPVCK 376

RESULT 28
O9FM98 PRELIMINARY; PRT; 396 AA.
ID O9FM98
AC O9FM98;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 5, PL CLONE:MCD7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:41-54(1998).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AB009049; BAB11261.1; -;
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger
SQ SEQUENCE 396 AA; 44359 MW; 43059E73B4442FFB CRC64;

Query Match 34.3%; Score 98; DB 10; Length 396;
Best Local Similarity 34.0%; Pred. No. 2.1e-05;

Matches 16; Conservative 10; Mismatches 19; Indels 2; Gaps 1;
OY 4 CTICSDFFDHSRDVAMDCGHTFHLCQCLIOSFETAPSTPCQCR 50
Db 259 CSVCLDFEKGCTEAKEMPCCKRHFVRCIVPWLIELHSS--CVCRRFL 303

RESULT 29
O9V978 PRELIMINARY; PRT; 621 AA.
ID O9V978
AC O9V978;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CG1937 PROTEIN.
GN CG1937.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyraoidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sultón G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burris R.C., Busam D.A., Butler H., Cadieu E., Cantier A., Chandra I.,
RA Cherry J.M., Cweley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöcker A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jbalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zhang R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AE003779; AAF57196.1; -;
DR FlyBase: FBgn0039875; CG1937.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger
SQ SEQUENCE 621 AA; 68752 MW; A8D6EB1609E2C0A1 CRC64;

Query Match 34.3%; Score 98; DB 5; Length 621;
Best Local Similarity 38.8%; Pred. No. 3.3e-05;
Matches 19; Conservative 8; Mismatches 16; Indels 6; Gaps 3;
OY 3 LCTIC-SDPFDHSDVAMDCGHTFHLCLOISFETAPSRRCPOCRIOV 50
DB 279 ICITICREDMNVNHSK---KLPCGHIFHTTCLRSWFOR--QQTCTPCRLNI 322

RESULT 30
OY95SP2 PRELIMINARY; PRT; 626 AA.
AC OY95SP2; 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN GH1111P.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN 11
SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Chante M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.,
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY060677; AAL28225.1; -
DR EMBL: AY060677; AAL28225.1; -
SQ SEQUENCE 626 AA; 69272 MW; F881B88D51D724EC CRC64;

Query Match 34.3%; Score 98; DB 5; Length 626;
Best Local Similarity 38.8%; Pred. No. 3.4e-05;
Matches 19; Conservative 8; Mismatches 16; Indels 6; Gaps 3;
OY 3 LCTIC-SDPFDHSDVAMDCGHTFHLCLOISFETAPSRRCPOCRIOV 50
DB 288 ICITICREDMNVNHSK---KLPCGHIFHTTCLRSWFOR--QQTCTPCRLNI 331

RESULT 31
OY95PB6 PRELIMINARY; PRT; 291 AA.
AC OY95PB6; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PGPD14 PROTEIN (AT5G22920/MRN17.15).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN 11
SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA.
RA MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Mayajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones."
RL DNA Res. 4:215-230(1997).
RN 12
SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koeseema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AB005243; BAB10613.1; -
DR EMBL: AY052362; AAK96553.1; -
DR InterPro: IPR000345; CYTC_heme_bind.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00097; zf-C3HC4.1.
DR SMART: SM00184; RING.1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
KM Zinc-finger.
SQ SEQUENCE 291 AA; 33549 MW; A54E62844ED93A66 CRC64;

Query Match 33.9%; Score 97; DB 10; Length 291;
Best Local Similarity 38.6%; Pred. No. 2.1e-05;
Matches 17; Conservative 8; Mismatches 17; Indels 2; Gaps 2;
OY 4 CTICSDP-FDHSRDVAMDCGHTFHLCLOISFETAPSRRCPOC 46
DB 163 CPVCFEYLFSDTRDITVLCGHTMHLCC-TKDMGLHNRITCPVC 205

RESULT 32
OY95PO5 PRELIMINARY; PRT; 243 AA.
AC OY95PO5; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TRIPARTITE MOTIF PROTEIN TRIM7.
GN TRIM7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN 11
SEQUENCE FROM N.A.
RX MEDLINE=21231161; PubMed=11331580;
RA Raymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L.,
RA Riganello D., Zanaria E., Messali S., Caimarca S., Guiffanti A.,
RA Minucci S., Pellici P.G., Balabio A.;
RT "The tripartite motif family identifies cell compartments."
RL EMBL J. 20:2140-2151(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF220033; AAG53487.1; -
DR HSSP: P15919; IRMD.
DR MGD: MGI:2137353; Trim7.
DR InterPro: IPR000315; ZnF-box.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00643; zf-B-box.1.
DR Pfam: PF00097; zf-C3HC4.1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00336; BBOX.1.
DR SMART: SM00184; RING.1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4.1.
KM Zinc-finger.
SQ SEQUENCE 243 AA; 27256 MW; 284F3D48B8BEC781 CRC64;

Query Match 33.7%; Score 96.5; DB 11; Length 243;
Best Local Similarity 32.8%; Pred. No. 2.1e-05;
Matches 19; Conservative 12; Mismatches 12; Indels 15; Gaps 2;
OY 2 ALCTICSDPFDHSDVAMDCGHTFHLCLOISFETAPSRRCPOCR 47
DB 27 ATCTICLERF---REPVSVECHSFCRACIMKWERPAGGTATRTPLPCPLPCPCR 81

RESULT 33
 094GW2 PRELIMINARY: PRT: 439 AA.
 AC 094GW2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE VIP2 PROTEIN.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M., Lee P.-F.,
 RA Su C.-L., Chen C.-S., Shaw J.-F.;
 RA "Oryza sativa PAC P0431G05 genomics sequence."
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AC087551; AAK70903.1; -
 DR SEQUENCE 439 AA; 47922 MW; A6707375E3260893 CRC64;
 SQ

Query Match 33.7%; Score 96.5; DB 10; Length 439;
 Best Local Similarity 38.3%; Pred. No. 3.8e-05;
 Matches 18; Conservative 4; Mismatches 22; Indels 3; Gaps 1;

QY 4 CTICSDPF---DHSRDVAMDCGHTFHLCLOISFETAPSRTPCPCR 47
 |||||
 DB 35 CSICIDAVVAAGGERSTARLQCGHEFHLCISAFNAKGVMOCPNCR 81

RESULT 34
 09MAC5 PRELIMINARY: PRT: 442 AA.
 AC 09MAC5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE VIP2 PROTEIN.
 GN VIP2.
 OS Avena fatua.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Poaceae; Avena.
 OX NCBI_TaxID=4499;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20208057; PubMed-10743654;
 RA Jones H.D., Kutup S., Peters N.C.B., Holdsworth M.J.;
 RT "Identification and analysis of proteins that interact with the Avena
 fatua homologue of the maize transcription factor VIVIPAROUS 1."
 RL Plant J. 21:133-142(2000).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AJ251051; CAB75506.1; -
 DR TRANSFAC: T04621; -
 DR InterPro: IPR001841; Znf_Ting.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00449; SPRY; 1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 DR ZINC_Finger.
 FT NON_TER
 SQ SEQUENCE 442 AA; 48184 MW; 441785914547281B CRC64;
 SO

Query Match 33.6%; Score 96; DB 10; Length 442;
 Best Local Similarity 37.5%; Pred. No. 4.4e-05;
 Matches 18; Conservative 4; Mismatches 22; Indels 4; Gaps 1;

QY 4 CTICSDPF---DHSRDVAMDCGHTFHLCLOISFETAPSRTPCPCR 47
 |||||
 DB 33 CSICIDAVVAAGGERSTARLQCGHEFHLCISAFNAKGVMOCPNCR 80

RESULT 35
 09UPQ4 PRELIMINARY: PRT: 504 AA.
 AC 09UPQ4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KIA1098 PROTEIN (FRAGMENT).
 GN KIA1098.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE-9397452; PubMed-10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro."
 RL DNA Res. 6:197-205(1999).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AB029021; BAA83050.1; -
 DR InterPro: IPR001870; Gamma_carboxylase.
 DR InterPro: IPR003877; SPRY.
 DR InterPro: IPR003877; SPRY.
 DR InterPro: IPR003877; SPRY.
 DR InterPro: IPR003877; SPRY.
 DR Pfam: PF00642; SPRY; 1.
 DR Pfam: PF00643; zf-B_box; 1.
 DR Pfam: PF00643; zf-B_box; 1.
 DR Pfam: PF00643; zf-B_box; 1.
 DR Pfam: PF00643; zf-B_box; 1.
 DR SMART: SM00336; BBOX; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00449; SPRY; 1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 DR ZINC_Finger.
 FT NON_TER
 SQ SEQUENCE 504 AA; 57735 MW; E0B377F32A36D1B9 CRC64;
 SO

Query Match 33.4%; Score 95.5; DB 4; Length 504;
 Best Local Similarity 40.0%; Pred. No. 6e-05;
 Matches 18; Conservative 6; Mismatches 18; Indels 3; Gaps 1;

QY 3 LCTICSDPFDSRDVAMDCGHTFHLCLOISFETAPSRTPCPCR 47
 |||||
 DB 31 LCAVCIDPF---RDVATLRCGHCRCGVCRCWCVQVSPCTPCVCK 72

RESULT 36
 09M143 PRELIMINARY: PRT: 506 AA.
 AC 09M143;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE RING ZINC FINGER PROTEIN.
 GN ATG01270.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamer B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL

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CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR      EMBL; AL161491; CAB80936.1; -
DR      InterPro: IPR001841; ZnF_fing.
DR      Pfam: PF00097; zf-C3HC4; 1.
DR      SMART: SM00184; RING; 1.
KW      Zinc-finger.
SQ      SEQUENCE 506 AA; 56518 MW; 1B06751A4E299FE8 CRC64;

Query Match
Best Local Similarity 33.4%; Score 95.5; DB 10; Length 506;
Matches 21; Conservative 9; Mismatches 14; Indels 9; Gaps 3;

OY      2 ALCTTSD----FFDHSRDVAAMDCGPHLQCLIOSFETAPS--RTCPQCR 47
DB      10 AICISCEYEDLKPYENVLQSIISA--CGHVFHELCLIQWFEYCPSTNKRMCPICK 60

RESULT 37
O92V08 PRELIMINARY; PRT; 351 AA.
AC      092V08:
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE      T5A14.7 PROTEIN (AT1G55530/T5A14_7).
GN      T5A14.7.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Federici N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA      Alatafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA      Gonzalez A., Kremenskaia I., Kim C., Lenz C., Li J., Liu S.,
RA      Luros S., Schwartz J., Shin P., Toriumi M., Vysotskaia V.S.,
RA      Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RA      Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA      Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA      Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA      Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA      Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA      Satou M., Seki M., Southwick A., Southwick A., Toriumi M., Yamada K.,
RA      Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
RA      Ecker J.R.;
RA      "Arabidopsis cDNA clones.";
RA      Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA      Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A.,
RA      Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,
RA      Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,
RA      Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA      Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA      Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinzaki K.,
RA      Davis R.W., Theologis A., Ecker J.R.;
RA      "Arabidopsis cDNA clones.";
RA      Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC      EMBL; AC005223; RAD10644.1; -
CC      EMBL; AF424578; AAL11572.1; -
CC      EMBL; AY03608; AAK62663.1; -
DR      InterPro: IPR001841; ZnF_fing.
DR      Pfam: PF00097; zf-C3HC4; 1.
DR      SMART: SM00184; RING; 1.
KW      Zinc-finger.
SQ      SEQUENCE 351 AA; 38963 MW; D55ABB4D72CFE7075 CRC64;

Query Match
Best Local Similarity 33.2%; Score 95; DB 10; Length 351;
Matches 18; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

OY      4 CTICSDFFDHSRDVAAMDCGPHLQCLIOSFETAPSRTCPQCRIOY 50
DB      85 CTICLSTLEGGEDVRRRLPCWHLFHVQVCDQWLIT--NKKCPICRVDI 129

RESULT 39
O942E6 PRELIMINARY; PRT; 299 AA.
AC      0942E6:
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE      PUTATIVE PEPD14 PROTEIN (POLLEN GERMINATION RELATED PROTEIN).
GN      P0480C01.20.
OS      Oryza sativa (Rice).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaeae; Oryza.
OX      NCBI_TaxID=4530;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN-CV. NIPPONBARE;
RA      Sasaki T., Matsumoto T., Yamamoto K.;
RA      "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RA      clone: P0480C01.";
SQ      SEQUENCE 351 AA; 38963 MW; D55ABB4D72CFE7075 CRC64;

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